

10/535325

WO 2004/045563

PCT/US2003/037653

Rec'd PCT/PTO 18 MAY 2005

- 1 -

SEQUENCE LISTING

<110> The Scripps Research Institute

Cheresh, David A.
Paul, Robert
Eliceiri, Brian

<120> Method of Treatment of Myocardial
Infarction

<130> TSRI-651.6

<150> 10/298,377
<151> 2002-11-18

<150> 09/538,248
<151> 2000-03-29

<150> 09/470,881
<151> 1999-12-22

<150> PCT/US99/11780
<151> 1999-05-28

<150> 60/087,220
<151> 1998-05-29

<160> 4

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 2187
<212> DNA
<213> homo sapiens

<220>
<221> CDS
<222> (134) ... (1486)

<400> 1
gcgcgcgcgc cccgaggccg tggatggccgc cggcgccggagg tggcccgac cgcagtgccc 60
caagagagct ctaatggta ccaatgtac caagtacacag gttggcttta ctgtgactcg gggacgcccag 120
agctcctgag aag atg tca gca ata cag gcc tgg cca tcc ggt aca 169
Met Ser Ala Ile Gln Ala Ala Trp Pro Ser Gly Thr
1 5 10

gaa tgt att gcc aag tac aac ttc cac ggc act gcc gag cag gac ctg 217
Glu Cys Ile Ala Lys Tyr Asn Phe His Gly Thr Ala Glu Gln Asp Leu
15 20 25

ccc ttc tgc aaa gga gac gtg ctc acc att gtg gcc gtc acc aag gac 265

- 2 -

Pro	Phe	Cys	Lys	Gly	Asp	Val	Leu	Thr	Ile	Val	Ala	Val	Thr	Lys	Asp	
30						35				40						
ccc	aac	tgg	tac	aaa	gcc	aaa	aac	aag	gtg	ggc	cgt	gag	ggc	atc	atc	313
Pro	Asn	Trp	Tyr	Lys	Ala	Lys	Asn	Lys	Val	Gly	Arg	Glu	Gly	Ile	Ile	
45					50					55				60		
cca	gcc	aac	tac	gtc	cag	aag	cgg	gag	ggc	gtg	aag	gct	ggt	acc	aaa	361
Pro	Ala	Asn	Tyr	Val	Gln	Lys	Arg	Glu	Gly	Val	Lys	Ala	Gly	Thr	Lys	
					65					70				75		
ctc	agc	ctc	atg	cct	tgg	ttc	cac	ggc	aag	atc	aca	cgg	gag	cag	gct	409
Leu	Ser	Leu	Met	Pro	Trp	Phe	His	Gly	Lys	Ile	Thr	Arg	Glu	Gln	Ala	
					80					85				90		
gag	cgg	ctt	ctg	tac	ccg	ccg	gag	aca	ggc	ctg	ttc	ctg	gtg	cgg	gag	457
Glu	Arg	Leu	Leu	Tyr	Pro	Pro	Glu	Thr	Gly	Leu	Phe	Leu	Val	Arg	Glu	
					95					100				105		
agc	acc	aac	tac	ccc	gga	gac	tac	acg	ctg	tgc	gtg	agc	tgc	gac	ggc	505
Ser	Thr	Asn	Tyr	Pro	Gly	Asp	Tyr	Thr	Leu	Cys	Val	Ser	Cys	Asp	Gly	
					110					115				120		
aag	gtg	gag	cac	tac	cgc	atc	atg	tac	cat	gcc	agc	aag	ctc	agc	atc	553
Lys	Val	Glu	His	Tyr	Arg	Ile	Met	Tyr	His	Ala	Ser	Lys	Leu	Ser	Ile	
					125					130				135		
gac	gag	gag	gtg	tac	ttt	gag	aac	ctc	atg	cag	ctg	gtg	gag	cac	tac	601
Asp	Glu	Glu	Val	Tyr	Phe	Glu	Asn	Leu	Met	Gln	Leu	Val	Glu	His	Tyr	
					145					150				155		
acc	tca	gac	gca	gat	gga	ctc	tgt	acg	cgc	ctc	att	aaa	cca	aag	gtc	649
Thr	Ser	Asp	Ala	Asp	Gly	Leu	Cys	Thr	Arg	Leu	Ile	Lys	Pro	Lys	Val	
					160					165				170		
atg	gag	ggc	aca	gtg	gct	gcc	cag	gat	gag	ttc	tac	cgc	agc	ggc	tgg	697
Met	Glu	Gly	Thr	Val	Ala	Ala	Gln	Asp	Glu	Phe	Tyr	Arg	Ser	Gly	Trp	
					175					180				185		
gcc	ctg	aac	atg	aag	gag	ctg	aag	ctg	ctg	cag	acc	atc	ggg	aag	ggg	745
Ala	Leu	Asn	Met	Lys	Glu	Leu	Lys	Leu	Leu	Gln	Thr	Ile	Gly	Lys	Gly	
					190					195				200		
gag	ttc	gga	gac	gtg	atg	ctg	ggc	gat	tac	cga	ggg	aac	aaa	gtc	gcc	793
Glu	Phe	Gly	Asp	Val	Met	Leu	Gly	Asp	Tyr	Arg	Gly	Asn	Lys	Val	Ala	
					205					210				215		
gtc	aag	tgc	att	aag	aac	gac	gcc	act	gcc	cag	gcc	ttc	ctg	gct	gaa	841
Val	Lys	Cys	Ile	Lys	Asn	Asp	Ala	Thr	Ala	Gln	Ala	Phe	Leu	Ala	Glu	
					225					230				235		
gcc	tca	gtc	atg	acg	caa	ctg	cg	cat	agc	aac	ctg	gtg	cag	ctc	ctg	889
Ala	Ser	Val	Met	Thr	Gln	Leu	Arg	His	Ser	Asn	Leu	Val	Gln	Leu	Leu	

- 3 -

240

245

250

ggc gtg atc gtg gag gag aag ggc ggg ctc tac atc gtc act gag tac 937
 Gly Val Ile Val Glu Glu Lys Gly Gly Leu Tyr Ile Val Thr Glu Tyr
 255 260 265

atg gcc aag ggg agc ctt gtg gac tac ctg cgg tct agg ggt cgg tca 985
 Met Ala Lys Gly Ser Leu Val Asp Tyr Leu Arg Ser Arg Gly Arg Ser
 270 275 280

gtg ctg ggc gga gac tgt ctc ctc aag ttc tcg cta gat gtc tgc gag 1033
 Val Leu Gly Gly Asp Cys Leu Leu Lys Phe Ser Leu Asp Val Cys Glu
 285 290 295 300

gcc atg gaa tac ctg gag ggc aac aat ttc gtg cat cga gac ctg gct 1081
 Ala Met Glu Tyr Leu Glu Gly Asn Asn Phe Val His Arg Asp Leu Ala
 305 310 315

gcc cgc aat gtg ctg gtg tct gag gac aac gtg gcc aag gtc agc gac 1129
 Ala Arg Asn Val Leu Val Ser Glu Asp Asn Val Ala Lys Val Ser Asp
 320 325 330

ttt ggt ctc acc aag gag gcg tcc agc acc cag gac acg ggc aag ctg 1177
 Phe Gly Leu Thr Lys Glu Ala Ser Ser Thr Gln Asp Thr Gly Lys Leu
 335 340 345

cca gtc aag tgg aca gcc cct gag gcc ctg aga gag aag aaa ttc tcc 1225
 Pro Val Lys Trp Thr Ala Pro Glu Ala Leu Arg Glu Lys Lys Phe Ser
 350 355 360

act aag tct gac gtg tgg agt ttc gga atc ctt ctc tgg gaa atc tac 1273
 Thr Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu Trp Glu Ile Tyr
 365 370 375 380

tcc ttt ggg cga gtg cct tat cca aga att ccc ctg aag gac gtc gtc 1321
 Ser Phe Gly Arg Val Pro Tyr Pro Arg Ile Pro Leu Lys Asp Val Val
 385 390 395

cct cgg gtg gag aag ggc tac aag atg gat gcc ccc gac ggc tgc ccg 1369
 Pro Arg Val Glu Lys Gly Tyr Lys Met Asp Ala Pro Asp Gly Cys Pro
 400 405 410

ccc gca gtc tat gaa gtc atg aag aac tgc tgg cac ctg gac gcc gcc 1417
 Pro Ala Val Tyr Glu Val Met Lys Asn Cys Trp His Leu Asp Ala Ala
 415 420 425

atg cgg ccc tcc ttc cta cag ctc cga gag cag ctt gag cac atc aaa 1465
 Met Arg Pro Ser Phe Leu Gln Leu Arg Glu Gln Leu Glu His Ile Lys
 430 435 440

acc cac gag ctg cac ctg tga cggctggcct ccgcctgggt catgggcctg 1516
 Thr His Glu Leu His Leu *
 445 450

- 4 -

tggggactga acctggaaga tcatggacct ggtgcccctg ctcactgggc ccgagcctga 1576
 actgagcccc agcgggctgg cgggccttt tcctgcgtcc cagcctgcac ccctccggcc 1636
 ccgtctctct tggaccacc tggggggct ggggagccca ctgaggggccc agggagggaaag 1696
 gaggccacgg agcgggaggc agcggccac cacgtcggc ttccctggcc tcccgccact 1756
 cgccttctta gagttttatt cctttccctt tttgagattt ttttccgtg tgtttatttt 1816
 ttattatttt tcaagataag gagaaagaaa gtacccagca aatgggcatt ttacaagaag 1876
 tacgaatctt attttcctg tccctgcctgt gagggtgggg gggaccgggc ccctctctag 1936
 ggaccctcg ccccagcctc attccccatt ctgtgtccca tgcccgtgt ctccctcggtc 1996
 gccccgtgt tgcgcttgac catgttgcac tggggcatg cggccgaggc agacgtctgt 2056
 caggggcttg gatttcgtgt gccgctgcca cccgcccacc cgcctgtga gatgaaattg 2116
 taataaaacca cgccatgagg acaccgcgc cgcctcgcc gcttcctcca ccgaaaaaaaa 2176
 aaaaaaaaaa a 2187

<210> 2
 <211> 450
 <212> PRT
 <213> homo sapiens

<400> 2
 Met Ser Ala Ile Gln Ala Ala Trp Pro Ser Gly Thr Glu Cys Ile Ala
 1 5 10 15
 Lys Tyr Asn Phe His Gly Thr Ala Glu Gln Asp Leu Pro Phe Cys Lys
 20 25 30
 Gly Asp Val Leu Thr Ile Val Ala Val Thr Lys Asp Pro Asn Trp Tyr
 35 40 45
 Lys Ala Lys Asn Lys Val Gly Arg Glu Gly Ile Ile Pro Ala Asn Tyr
 50 55 60
 Val Gln Lys Arg Glu Gly Val Lys Ala Gly Thr Lys Leu Ser Leu Met
 65 70 75 80
 Pro Trp Phe His Gly Lys Ile Thr Arg Glu Gln Ala Glu Arg Leu Leu
 85 90 95
 Tyr Pro Pro Glu Thr Gly Leu Phe Leu Val Arg Glu Ser Thr Asn Tyr
 100 105 110
 Pro Gly Asp Tyr Thr Leu Cys Val Ser Cys Asp Gly Lys Val Glu His
 115 120 125
 Tyr Arg Ile Met Tyr His Ala Ser Lys Leu Ser Ile Asp Glu Glu Val
 130 135 140
 Tyr Phe Glu Asn Leu Met Gln Leu Val Glu His Tyr Thr Ser Asp Ala
 145 150 155 160
 Asp Gly Leu Cys Thr Arg Leu Ile Lys Pro Lys Val Met Glu Gly Thr
 165 170 175
 Val Ala Ala Gln Asp Glu Phe Tyr Arg Ser Gly Trp Ala Leu Asn Met
 180 185 190
 Lys Glu Leu Lys Leu Leu Gln Thr Ile Gly Lys Gly Glu Phe Gly Asp
 195 200 205
 Val Met Leu Gly Asp Tyr Arg Gly Asn Lys Val Ala Val Lys Cys Ile
 210 215 220
 Lys Asn Asp Ala Thr Ala Gln Ala Phe Leu Ala Glu Ala Ser Val Met
 225 230 235 240
 Thr Gln Leu Arg His Ser Asn Leu Val Gln Leu Leu Gly Val Ile Val
 245 250 255
 Glu Glu Lys Gly Gly Leu Tyr Ile Val Thr Glu Tyr Met Ala Lys Gly

- 5 -

260	265	270
Ser Leu Val Asp Tyr Leu Arg Ser Arg Gly Arg Ser Val	Leu Gly Gly	
275	280	285
Asp Cys Leu Leu Lys Phe Ser Leu Asp Val Cys Glu Ala Met Glu Tyr		
290	295	300
Leu Glu Gly Asn Asn Phe Val His Arg Asp Leu Ala Ala Arg Asn Val		
305	310	315
Leu Val Ser Glu Asp Asn Val Ala Lys Val Ser Asp Phe Gly Leu Thr		
325	330	335
Lys Glu Ala Ser Ser Thr Gln Asp Thr Gly Lys Leu Pro Val Lys Trp		
340	345	350
Thr Ala Pro Glu Ala Leu Arg Glu Lys Lys Phe Ser Thr Lys Ser Asp		
355	360	365
Val Trp Ser Phe Gly Ile Leu Leu Trp Glu Ile Tyr Ser Phe Gly Arg		
370	375	380
Val Pro Tyr Pro Arg Ile Pro Leu Lys Asp Val Val Pro Arg Val Glu		
385	390	395
Lys Gly Tyr Lys Met Asp Ala Pro Asp Gly Cys Pro Pro Ala Val Tyr		
405	410	415
Glu Val Met Lys Asn Cys Trp His Leu Asp Ala Ala Met Arg Pro Ser		
420	425	430
Phe Leu Gln Leu Arg Glu Gln Leu Glu His Ile Lys Thr His Glu Leu		
435	440	445
His Leu		
450		

<210> 3

<211> 4517

<212> DNA

<213> homo sapiens

<220>

<221> CDS

<222> (208) ... (1839)

<400> 3

gcggagccaa ggcacacggg tctgaccctt gggccggccc ggagcaagtg acacggacccg	60
gtcgctatac ctgaccacag caaagcggcc cggagcccgcc ggaggggacc tgacgggggc	120
gtaggcgccg gaaggctggg ggccccggag cggggccggc gtggcccgag ttccgggtgag	180
cggacggcgg cgcgcgacata tttgata atg ggc tgc att aaa agt aaa gaa aac	234
Met Gly Cys Ile Lys Ser Lys Glu Asn	
1	5

aaa agt cca gcc att aaa tac aga cct gaa aat act cca gag cct gtc	282		
Lys Ser Pro Ala Ile Lys Tyr Arg Pro Glu Asn Thr Pro Glu Pro Val			
10	15	20	25

agt aca agt gtg agc cat tat gga gca gaa ccc act aca gtg tca cca	330		
Ser Thr Ser Val Ser His Tyr Gly Ala Glu Pro Thr Thr Val Ser Pro			
30	35	40	

tgt ccg tca tct tca gca aag gga aca gca gtt aat ttc agc agt ctt	378
---	-----

- 6 -

Cys Pro Ser Ser Ser Ala Lys Gly Thr Ala Val Asn Phe Ser Ser Leu		
45	50	55
tcc atg aca cca ttt gga gga tcc tca ggg gta acg cct ttt gga ggt 426		
Ser Met Thr Pro Phe Gly Gly Ser Ser Gly Val Thr Pro Phe Gly Gly		
60	65	70
gca tct tcc tca ttt tca gtg gtg cca agt tca tat cct gct ggt tta 474		
Ala Ser Ser Ser Phe Ser Val Val Pro Ser Ser Tyr Pro Ala Gly Leu		
75	80	85
aca ggt ggt gtt act ata ttt gtg gcc tta tat gat tat gaa gct aga 522		
Thr Gly Gly Val Thr Ile Phe Val Ala Leu Tyr Asp Tyr Glu Ala Arg		
90	95	100
act aca gaa gac ctt tca ttt aag aag ggt gaa aga ttt caa ata att 570		
Thr Thr Glu Asp Leu Ser Phe Lys Lys Gly Glu Arg Phe Gln Ile Ile		
110	115	120
aac aat acg gaa gga gat tgg tgg gaa gca aga tca atc gct aca gga 618		
Asn Asn Thr Glu Asp Trp Trp Glu Ala Arg Ser Ile Ala Thr Gly		
125	130	135
aag aat ggt tat atc ccg agc aat tat gta gcg cct gca gat tcc att 666		
Lys Asn Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Ala Asp Ser Ile		
140	145	150
cag gca gaa gaa tgg tat ttt ggc aaa atg ggg aga aaa gat gct gaa 714		
Gln Ala Glu Glu Trp Tyr Phe Gly Lys Met Gly Arg Lys Asp Ala Glu		
155	160	165
aga tta ctt ttg aat cct gga aat caa cga ggt att ttc tta gta aga 762		
Arg Leu Leu Leu Asn Pro Gly Asn Gln Arg Gly Ile Phe Leu Val Arg		
170	175	180
gag agt gaa aca act aaa ggt gct tat tcc ctt tct att cgt gat tgg 810		
Glu Ser Glu Thr Thr Lys Gly Ala Tyr Ser Leu Ser Ile Arg Asp Trp		
190	195	200
gat gag ata agg ggt gac aat gtg aaa cac tac aaa att agg aaa ctt 858		
Asp Glu Ile Arg Gly Asp Asn Val Lys His Tyr Lys Ile Arg Lys Leu		
205	210	215
gac aat ggt gga tac tat atc aca acc aga gca caa ttt gat act ctg 906		
Asp Asn Gly Gly Tyr Tyr Ile Thr Thr Arg Ala Gln Phe Asp Thr Leu		
220	225	230
cag aaa ttg gtg aaa cac tac aca gaa cat gct gat ggt tta tgc cac 954		
Gln Lys Leu Val Lys His Tyr Thr Glu His Ala Asp Gly Leu Cys His		
235	240	245
aag ttg aca act gtg tgt cca act gtg aaa cct cag act caa ggt cta 1002		
Lys Leu Thr Thr Val Cys Pro Thr Val Lys Pro Gln Thr Gln Gly Leu		

- 7 -

250	255	260	265	
gca aaa gat gct tgg gaa atc cct cga gaa tct ttg cga cta gag gtt				1050
Ala Lys Asp Ala Trp Glu Ile Pro Arg Glu Ser Leu Arg Leu Glu Val				
270	275	280		
aaa cta gga caa gga tgt ttc ggc gaa gtg tgg atg gga aca tgg aat				1098
Lys Leu Gly Gln Gly Cys Phe Gly Glu Val Trp Met Gly Thr Trp Asn				
285	290	295		
gga acc acg aaa gta gca atc aaa aca cta aaa cca ggt aca atg atg				1146
Gly Thr Thr Lys Val Ala Ile Lys Thr Leu Lys Pro Gly Thr Met Met				
300	305	310		
cca gaa gct ttc ctt caa gaa gct cag ata atg aaa aaa tta aga cat				1194
Pro Glu Ala Phe Leu Gln Glu Ala Gln Ile Met Lys Lys Leu Arg His				
315	320	325		
gat aaa ctt gtt cca cta tat gct gtt gtt tct gaa gaa cca att tac				1242
Asp Lys Leu Val Pro Leu Tyr Ala Val Val Ser Glu Glu Pro Ile Tyr				
330	335	340	345	
att gtc act gaa ttt atg tca aaa gga agc tta tta gat ttc ctt aag				1290
Ile Val Thr Glu Phe Met Ser Lys Gly Ser Leu Leu Asp Phe Leu Lys				
350	355	360		
gaa gga gat gga aag tat ttg aag ctt cca cag ctg gtt gat atg gct				1338
Glu Gly Asp Gly Lys Tyr Leu Lys Leu Pro Gln Leu Val Asp Met Ala				
365	370	375		
gct cag att gct gat ggt atg gca tat att gaa aga atg aac tat att				1386
Ala Gln Ile Ala Asp Gly Met Ala Tyr Ile Glu Arg Met Asn Tyr Ile				
380	385	390		
cac cga gat ctt cg ^g gct gct aat att ctt gta gga gaa aat ctt gt ^g				1434
His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val Gly Glu Asn Leu Val				
395	400	405		
tgc aaa ata gca gac ttt ggt tta gca agg tta att gaa gac aat gaa				1482
Cys Lys Ile Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu Asp Asn Glu				
410	415	420	425	
tac aca gca aga caa ggt gca aaa ttt cca atc aaa tgg aca gct cct				1530
Tyr Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp Thr Ala Pro				
430	435	440		
gaa gct gca ctg tat ggt cg ^g ttt aca ata aag tct gat gtc tgg tca				1578
Glu Ala Ala Leu Tyr Gly Arg Phe Thr Ile Lys Ser Asp Val Trp Ser				
445	450	455		
ttt gga att ctg caa aca gaa cta gta aca aag ggc cga gtg cca tat				1626
Phe Gly Ile Leu Gln Thr Glu Leu Val Thr Lys Gly Arg Val Pro Tyr				
460	465	470		

- 8 -

- 9 -

tttcaggat ataattctta actatcatta tttacctgat tttaatcatc agattcgaaa 3849
ttctgtgcca tggcgtataat gttcaattc aaaccattt taaaatgtga agatggactt 3909
catgcaagtt ggcagtgggt ctggtaactaa aaattgtggt tgtttttct gtttacgtaa 3969
cctgccttagt attgacactc tctaccaaga gggcttcct aagaagagtg ctgtcattat 4029
ttcctcttat caacaacttg tgacatgaga ttttttaagg gctttatgtg aactatgata 4089
ttgtaatttt tctaaggcata ttcaaaaaggg tgacaaaatt acgtttatgt actaaatcta 4149
atcaggaaag taaggcagga aaagtgtatg gtattcatta ggttttaact gaatggagca 4209
gttccttata taataacaat tgtatagtag ggataaaaaca ctaacaatgt gtattcattt 4269
taaattgttc tgtatttta aattgccaag aaaaacaact ttgtaaattt ggagatattt 4329
tccaacagct ttcgtcttc agtgtcttaa tgtggaaagtt aacccttacc aaaaaaggaa 4389
gttggcaaaa acagccttct agcacacttt tttaaatgaa taatggtagc ctaaacttaa 4449
tattttata aagtattgtta atattgtttt gtggataatt gaaataaaaaa gttctcattt 4509
aatgcacc 4517

<210> 4
<211> 543
<212> PRT
<213> homo sapiens

<400> 4
Met Gly Cys Ile Lys Ser Lys Glu Asn Lys Ser Pro Ala Ile Lys Tyr
1 5 10 15
Arg Pro Glu Asn Thr Pro Glu Pro Val Ser Thr Ser Val Ser His Tyr
20 25 30
Gly Ala Glu Pro Thr Thr Val Ser Pro Cys Pro Ser Ser Ser Ala Lys
35 40 45
Gly Thr Ala Val Asn Phe Ser Ser Leu Ser Met Thr Pro Phe Gly Gly
50 55 60
Ser Ser Gly Val Thr Pro Phe Gly Gly Ala Ser Ser Ser Phe Ser Val
65 70 75 80
Val Pro Ser Ser Tyr Pro Ala Gly Leu Thr Gly Gly Val Thr Ile Phe
85 90 95
Val Ala Leu Tyr Asp Tyr Glu Ala Arg Thr Thr Glu Asp Leu Ser Phe
100 105 110
Lys Lys Gly Glu Arg Phe Gln Ile Ile Asn Asn Thr Glu Gly Asp Trp
115 120 125
Trp Glu Ala Arg Ser Ile Ala Thr Gly Lys Asn Gly Tyr Ile Pro Ser
130 135 140
Asn Tyr Val Ala Pro Ala Asp Ser Ile Gln Ala Glu Glu Trp Tyr Phe
145 150 155 160
Gly Lys Met Gly Arg Lys Asp Ala Glu Arg Leu Leu Leu Asn Pro Gly
165 170 175
Asn Gln Arg Gly Ile Phe Leu Val Arg Glu Ser Glu Thr Thr Lys Gly
180 185 190
Ala Tyr Ser Leu Ser Ile Arg Asp Trp Asp Glu Ile Arg Gly Asp Asn
195 200 205
Val Lys His Tyr Lys Ile Arg Lys Leu Asp Asn Gly Gly Tyr Tyr Ile
210 215 220
Thr Thr Arg Ala Gln Phe Asp Thr Leu Gln Lys Leu Val Lys His Tyr
225 230 235 240
Thr Glu His Ala Asp Gly Leu Cys His Lys Leu Thr Thr Val Cys Pro
245 250 255
Thr Val Lys Pro Gln Thr Gln Gly Leu Ala Lys Asp Ala Trp Glu Ile

- 10 -

260	265	270
Pro Arg Glu Ser Leu Arg Leu Glu Val Lys Leu Gly Gln Gly Cys Phe		
275	280	285
Gly Glu Val Trp Met Gly Thr Trp Asn Gly Thr Thr Lys Val Ala Ile		
290	295	300
Lys Thr Leu Lys Pro Gly Thr Met Met Pro Glu Ala Phe Leu Gln Glu		
305	310	315
Ala Gln Ile Met Lys Lys Leu Arg His Asp Lys Leu Val Pro Leu Tyr		
325	330	335
Ala Val Val Ser Glu Glu Pro Ile Tyr Ile Val Thr Glu Phe Met Ser		
340	345	350
Lys Gly Ser Leu Leu Asp Phe Leu Lys Glu Gly Asp Gly Lys Tyr Leu		
355	360	365
Lys Leu Pro Gln Leu Val Asp Met Ala Ala Gln Ile Ala Asp Gly Met		
370	375	380
Ala Tyr Ile Glu Arg Met Asn Tyr Ile His Arg Asp Leu Arg Ala Ala		
385	390	395
Asn Ile Leu Val Gly Glu Asn Leu Val Cys Lys Ile Ala Asp Phe Gly		
405	410	415
Leu Ala Arg Leu Ile Glu Asp Asn Glu Tyr Thr Ala Arg Gln Gly Ala		
420	425	430
Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ala Leu Tyr Gly Arg		
435	440	445
Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Gln Thr Glu		
450	455	460
Leu Val Thr Lys Gly Arg Val Pro Tyr Pro Gly Met Val Asn Arg Glu		
465	470	475
Val Leu Glu Gln Val Glu Arg Gly Tyr Arg Met Pro Cys Pro Gln Gly		
485	490	495
Cys Pro Glu Ser Leu His Glu Leu Met Asn Leu Cys Trp Lys Lys Asp		
500	505	510
Pro Asp Glu Arg Pro Thr Phe Glu Tyr Ile Gln Ser Phe Leu Glu Asp		
515	520	525
Tyr Phe Thr Ala Thr Glu Pro Gln Tyr Gln Pro Gly Glu Asn Leu		
530	535	540